Amendments to the Specification:

Please insert the following new section, immediately after paragraph [0002].

STATEMENT REGARDING SEQUENCE LISTING

[0002a] The Sequence Listing associated with this application is provided in text format in lieu of a paper copy, and is hereby incorporated by reference into the specification. The name of the text file containing the Sequence Listing is 210121_579USPC_SEQUENCE_LISTING.txt. The text file is 67 KB, was created on November 30, 2010, and is being submitted electronically via EFS-Web.

Please replace paragraph [0056] with the following red-lined paragraph:

[0056] Another way to make amino acid substitutions to produce variants of the present invention is to identify and replace amino acids in T cell motifs with potential to bind to class II MHC molecules (for $CD4^+$ T cell response) or class I MHC molecules (for $CD8^+$ T cell response). Peptide segments with a motif with theoretical potential to bind to class II MHC molecules may be identified by computer analysis. For example, a protein sequence analysis package, *T Sites,* that incorporates several computer algorithms designed to distinguish potential sites for T cell recognition can be used (Feller *et al.* (1991) *Nature* 349:720-721). Two searching algorithms are used: (1) the AMPHI algorithm described by Margalit (Feller *et al.* (1991) *Nature* 349:720-721; Margalit *et al.* (1987) *J. Immunol.* 138:2213-2229) identifies epitope motifs according to alpha-helical periodicity and amphipathicity; (2) the Rothbard and Taylor algorithm identifies epitope motifs according to charge and polarity pattern (Rothbard *et al.* (1988) *EMBO J.* 7:93-100). Segments with both motifs are most appropriate for binding to class II MHC molecules. $CD8^+$ T cells recognize peptides bound to class I MHC molecules. Parker *et al.* (1994) *J. Immunol.* 152:163 have determined that peptides binding to particular MHC molecules share discernible sequence motifs. A peptide motif for binding in the groove of HLA-A2.1 has been defined by Edman degradation of peptides stripped from HLA-A2.l molecules of a cultured cell line (Table 1, from Falk *et al.* (1991) *Nature* 351:290-296). The method identified the typical or average HLA-A2.l binding peptide as being 9 amino acids in length with dominant

anchor residues occurring at positions 2 (L) and 9 (V) (SEQ ID NO:9). Commonly occurring strong binding residues have been identified at positions 2 (M), 4 (E,K), 6 (V), and 8 (K). The identified motif represents the average of many binding peptides.

Please replace paragraph [0057] with the following red-lined paragraph:

[0057] The derived peptide motif (SEQ ID NO:9) as currently defined is not particularly stringent. Some HLA-A2.1 binding peptides do not contain both dominant anchor residues and the amino acids flanking the dominant anchor residues play major roles in allowing or disallowing binding. Not every peptide with the current described binding motif will bind, and some peptides without the motif will bind. However, the current motif is valid enough to allow identification of some peptides capable of binding. Of note, all MHC molecules and respective motifs place 6 amino acids between the dominant anchor amino acids at residues 2 and 9.

Please delete the section of the application entitled "Sequence Listing" immediately after claim 25 on page 67.